wwPDB X-ray Structure Validation Summary Report (i)

Nov 19, 2023 – 05:30 PM JST

PDB ID	:	6LTP
Title	:	Crystal structure of Cas12i2 binary complex
Authors	:	Huang, X.; Sun, W.; Cheng, Z.; Chen, M.; Li, X.; Wang, J.; Sheng, G.; Gong, W.; Wang, Y.
Deposited on	:	2020-01-23
Resolution	:	3.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

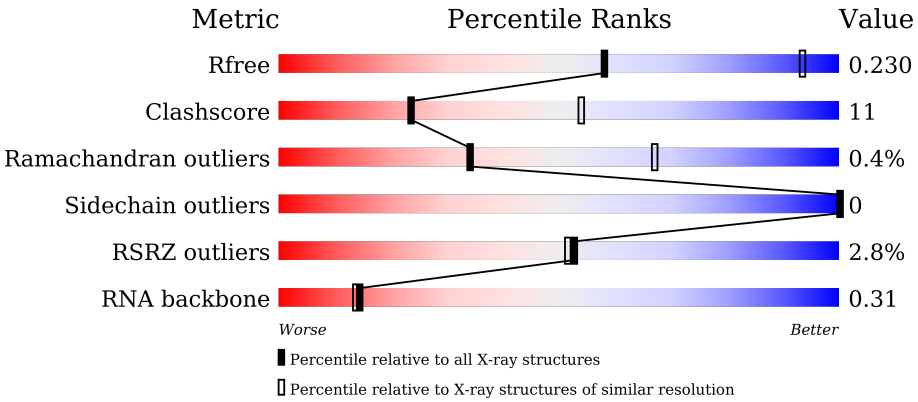
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)
RNA backbone	3102	1006 (3.84-2.96)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1055	3% 66% 21% 13%
1	G	1055	65% 21% · 13%
2	B	56	12% 23% 34% 18% 25%
2	H	56	11% 27% 30% 12% 5% 25%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 16382 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Cas12i2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	920	Total	C	N	O	S	0	0	0
			7244	4606	1267	1345	26			
1	G	923	Total	C	N	O	S	0	0	0
			7348	4681	1292	1349	26			

- Molecule 2 is a RNA chain called crRNA (56-mer RNA).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	42	Total	C	N	O	P	0	0	0
			889	400	157	291	41			
2	H	42	Total	C	N	O	P	0	0	0
			889	400	157	291	41			

- Molecule 3 is water.

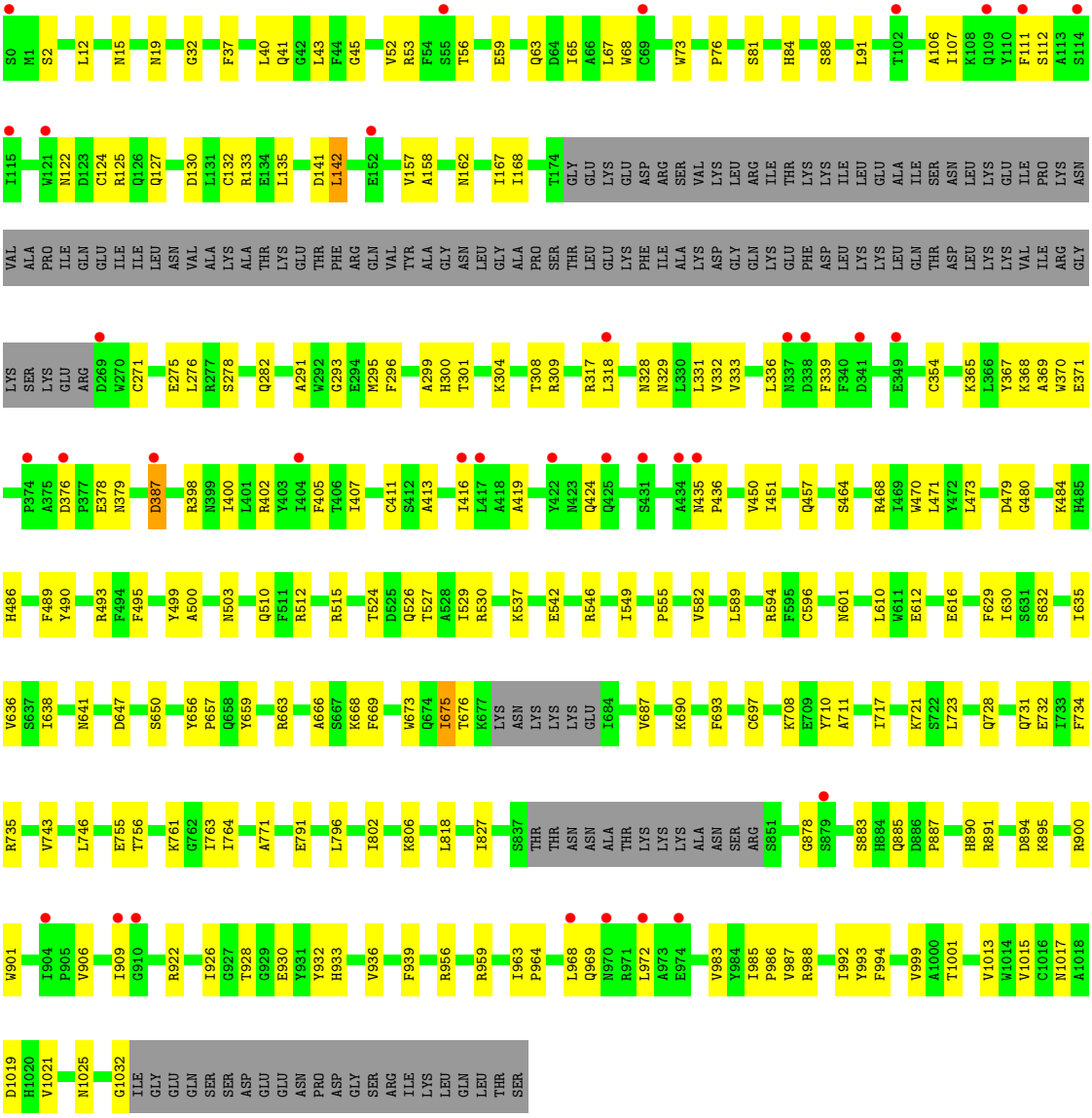
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	O	0	0
			4	4		
3	B	1	Total	O	0	0
			1	1		
3	G	7	Total	O	0	0
			7	7		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

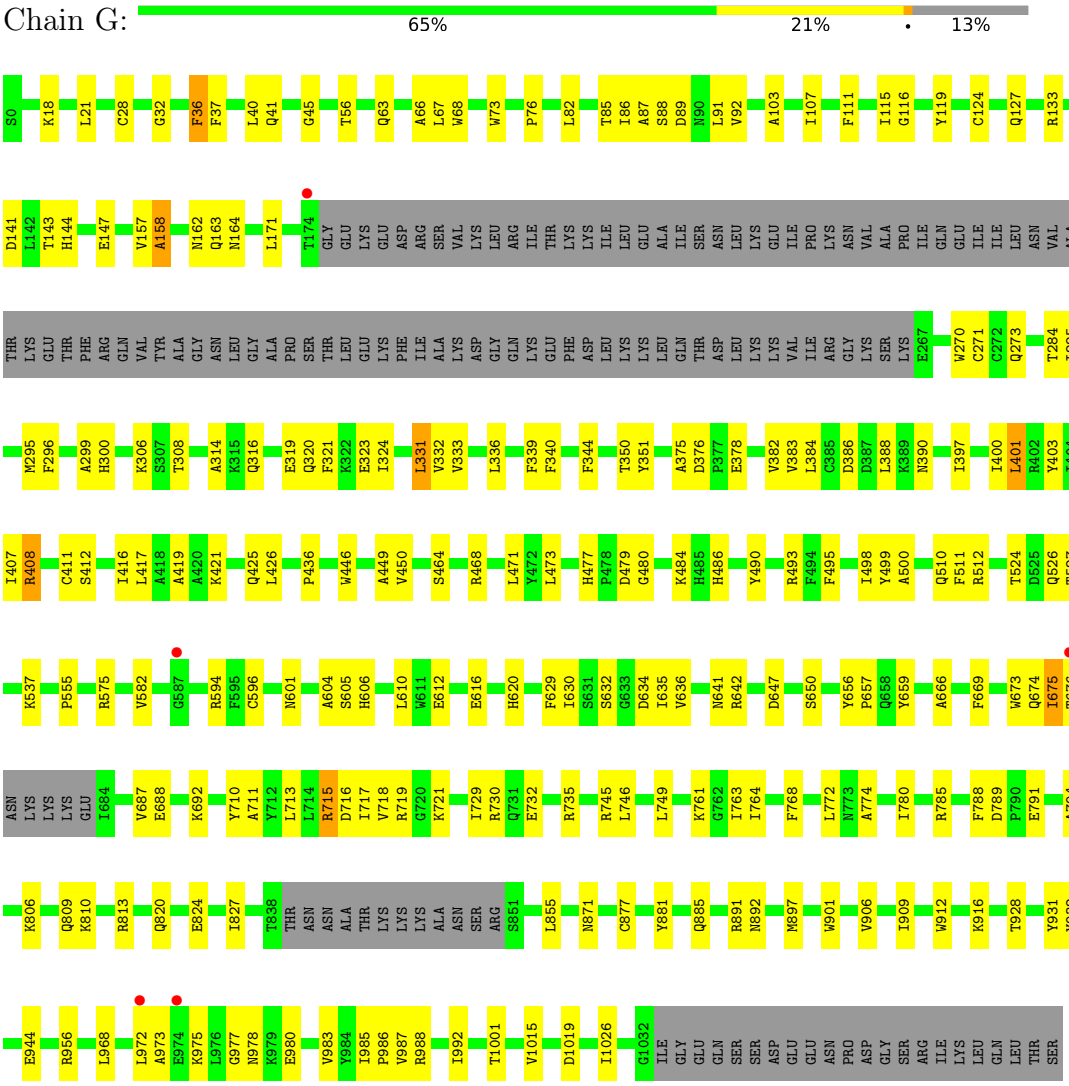
- Molecule 1: Cas12i2

Chain A:



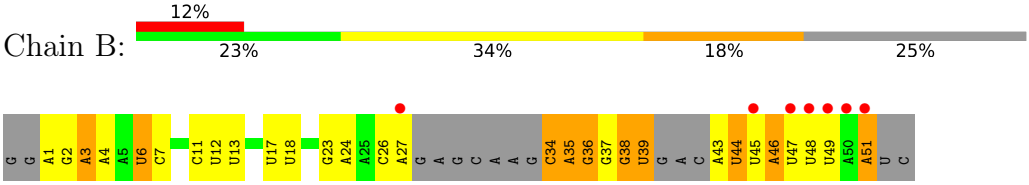
- Molecule 1: Cas12i2

Chain G:



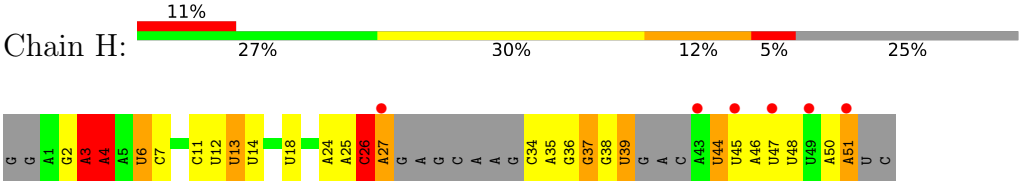
• Molecule 2: crRNA (56-mer RNA)

Chain B:



• Molecule 2: crRNA (56-mer RNA)

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	146.31Å 146.31Å 144.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.71 – 3.40 48.71 – 3.40	Depositor EDS
% Data completeness (in resolution range)	94.8 (48.71-3.40) 94.8 (48.71-3.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.01 (at 3.40Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.207 , 0.230 0.207 , 0.230	Depositor DCC
R_{free} test set	2151 reflections (5.42%)	wwPDB-VP
Wilson B-factor (Å^2)	48.4	Xtriage
Anisotropy	0.002	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 29.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	0.032 for -h,-l,-k 0.026 for -h,l,k 0.026 for l,-k,h 0.034 for -l,-k,-h 0.047 for h,-k,-l	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	16382	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.39% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.37	1/7399 (0.0%)	0.65	3/10025 (0.0%)
1	G	0.39	1/7505 (0.0%)	0.68	9/10154 (0.1%)
2	B	0.36	0/992	1.03	0/1538
2	H	0.39	0/992	1.11	3/1538 (0.2%)
All	All	0.38	2/16888 (0.0%)	0.73	15/23255 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	891	ARG	CZ-NH2	5.96	1.40	1.33
1	A	367	TYR	CE1-CZ	-5.10	1.31	1.38

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	142	LEU	CB-CG-CD2	-11.48	91.47	111.00
1	G	89	ASP	CB-CG-OD1	-10.60	108.76	118.30
1	G	634	ASP	CB-CG-OD1	-8.12	111.00	118.30
1	G	401	LEU	CB-CG-CD2	-6.85	99.35	111.00
1	G	408	ARG	NE-CZ-NH1	-6.39	117.11	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7244	0	6970	170	0
1	G	7348	0	7182	174	0
2	B	889	0	453	19	0
2	H	889	0	453	21	0
3	A	4	0	0	0	0
3	B	1	0	0	0	0
3	G	7	0	0	0	0
All	All	16382	0	15058	350	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 350 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:928:THR:HG23	1:G:988:ARG:HH22	1.06	1.13
1:G:715:ARG:HH21	1:G:719:ARG:HH21	1.07	0.95
1:A:376:ASP:HB2	1:A:379:ASN:HD21	1.34	0.91
1:G:692:LYS:HD3	1:G:713:LEU:HD13	1.51	0.90
1:G:928:THR:HG23	1:G:988:ARG:NH2	1.90	0.86

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	912/1055 (86%)	873 (96%)	37 (4%)	2 (0%)	47	78
1	G	915/1055 (87%)	867 (95%)	43 (5%)	5 (0%)	29	61
All	All	1827/2110 (87%)	1740 (95%)	80 (4%)	7 (0%)	34	67

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	675	ILE
1	G	412	SER
1	G	675	ILE
1	G	164	ASN
1	G	158	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	748/931 (80%)	748 (100%)	0	100	100
1	G	770/931 (83%)	770 (100%)	0	100	100
All	All	1518/1862 (82%)	1518 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	618	GLN
1	G	63	GLN
1	G	162	ASN
1	A	300	HIS
1	A	164	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	40/56 (71%)	18 (45%)	5 (12%)
2	H	40/56 (71%)	18 (45%)	5 (12%)
All	All	80/112 (71%)	36 (45%)	10 (12%)

5 of 36 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	2	G
2	B	3	A
2	B	6	U
2	B	13	U
2	B	18	U

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	H	35	A
2	H	37	G
2	H	47	U
2	B	36	G
2	B	47	U

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	920/1055 (87%)	0.19	35 (3%) 40 39	7, 52, 96, 122	0
1	G	923/1055 (87%)	-0.01	5 (0%) 91 90	8, 41, 89, 123	0
2	B	42/56 (75%)	0.45	7 (16%) 1 2	13, 41, 166, 175	0
2	H	42/56 (75%)	0.41	6 (14%) 2 3	10, 35, 167, 178	0
All	All	1927/2222 (86%)	0.10	53 (2%) 53 51	7, 46, 97, 178	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	102	THR	4.2
2	B	49	U	3.5
1	G	587	GLY	3.3
1	A	404	ILE	3.3
1	A	434	ALA	3.2

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.